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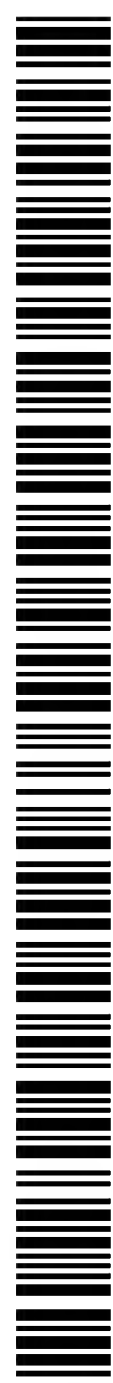
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(54) Title: METHOD FOR PREDICTING DE NOVO BIOMACROMOLECULE CRYSTALLIZATION CONDITIONS AND FOR CRYSTALLIZATION OF THE SAME

(57) Abstract: A method de novo is provided for predicting crystallization conditions and for crystallizing biomacromolecules, in particular proteins. The method provides a simple, quick and precise approach in determining the biomacromolecule solubility in different solutions, as well as the boundary between crystallization and aggregation. Because the method relies only on monitoring the assembly behavior of the biomacromolecule at the surface of a solution, it has general applicability and requires a relatively short amount of time to provide results that are reliable. Because there is no need to first crystallize the biomacromolecule, smaller amounts of protein suffice as compared with amounts required for crystallization. Because the method works by measuring the surface tension or surface pressure of the surface of the biomacromolecule solution, it is easy, precise and quick. Furthermore it is cost-effective in requiring simple and inexpensive equipment. Additionally, the method not only provides information on the solvent conditions where crystallization, rather than amorphous aggregation, takes place, but also on the critical equilibrium condition of the protein. This enables the user to restrict experimental parameters to protein concentrations above the equilibrium value, that are viable for crystallization.



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